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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=11; hr=16; min=0; sec=10; ms=848; ]

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Application No: 10650559 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-03-11 11:29:08.558  
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Total Warnings: 5  
Total Errors: 0  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

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| W 213      | Artificial or Unknown found in <213> in SEQ ID (5) |

# SEQUENCE LISTING

<110> Pritchard, David G.  
Baker, John R.  
Schwebke, Jane R.  
Engler, Jeffrey A.

<120> Group B Streptococcal Phage Lysin

<130> P66186US01GP

<140> 10650559

<141> 2008-03-11

<150> US 60/407,038

<151> 2002-08-29

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| gctgttactg taactgataa taccggttta aataaagggtg attactttat cgatgtatcg  | 480 |
| gcttatcaac aagcagatctt aacaacgact tgtcagcagg cgggcactac aaaaacgatt  | 540 |
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| gactatgaag attccgcaag cgcagacaag caagctaaca caaatgcagt tattgcattt   | 780 |
| atggataaaa tcgctagcgc tggatataag cctattttatt acagctataa accatttacg  | 840 |
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| caggcgggca ctacaaaaac gattatcaag gtatccgagt caattgcttg gctgtctgac  | 720  |
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| aacacaaatg cagttattgc atttatggat aaaatcgcta gcgctggata taagcctatt  | 960  |
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| tagttcttcc tcagaattta aacaaatata acattacgaa aatcgttacc aatttcaata  | 1680 |
| gattacttgc ttttaagtgat aacaggacac ttacagtaga tatgagaaac attgagtttg | 1740 |
| cggaacctag tggagtaatt tcgttatata atatgttaac ttttgctaca aaaagaaaag  | 1800 |
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Tyr Phe Asp Glu Val Glu Thr Met Gln Ala Gly Asp Val Ala Ile Phe  
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Met Val Val Ala Gly Val Thr Pro Tyr Ser His Val Ala Ile Phe Asp  
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Ser Asp Ala Gly Ser Gly Tyr Gly Trp Phe Leu Gly Gln Asn Gln Gly  
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Gly Ala Asn Gly Ala Tyr Asn Leu Val Lys Ile Pro Tyr Ser Thr Thr  
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Ala Tyr Gln Gln Ala Asp Leu Thr Ala Thr Cys Gln Gln Ala Gly Thr  
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Thr Lys Thr Ile Ile Lys Val Ser Glu Ser Leu Ala Trp Leu Ser Asp  
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Arg His Gln Gln Gln Ala Asn Thr Ser Asp Pro Ile Gly Tyr Tyr His  
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Phe Gly Arg Phe Gly Gly Asp Ser Asn Leu Ala Gln Arg Val Ala Asp  
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Asp Tyr Glu Asp Ser Ala Ser Ala Asp Lys Glu Ala Asn Thr Lys Ala  
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Val Ile Ala Phe Met Asp Lys Ile Ala Asn Ala Gly Tyr Lys Pro Val  
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Tyr Tyr Ser Tyr Lys Pro Phe Thr Leu Asn Asn Ile Asp Tyr Gln Gln  
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Ile Ile Ala Lys Tyr Pro Asn Ser Ile Trp Ile Ala Gly Tyr Pro Asp  
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Tyr Glu Val Arg Thr Glu Pro Leu Trp Glu Phe Phe Pro Ser Met Asp  
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345

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Pro Lys Ile Asp Lys Pro Gln Ser Gln Leu Thr Phe Asn Gln Lys Leu  
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Asp Thr Asn Thr Lys Leu Asp Asn Ser Asn Val Pro Tyr Tyr Glu Ala  
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Thr Leu Ser Thr Asp Tyr Tyr Val Glu Ser Lys Pro Asn Ala Ser Ser  
 385 390 395 400

Ala Asp Lys Glu Phe Ile Lys Ala Gly Thr Arg Val Arg Val Tyr Glu  
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Lys Val Asn Gly Trp Ser Arg Ile Asn Ala Ser Gln Ser Asp Gln Trp  
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Tyr Cys Lys Tyr Leu Gly Leu Pro Tyr Ala Asn Cys Thr Asn Thr Gly  
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Tyr Ala Lys Asp Ile Trp Glu Gln Arg His Lys Asn Gly Ile Leu Asn  
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Tyr Phe Asp Glu Val Glu Thr Met Gln Ala Gly Asp Val Ala Ile Phe  
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Met Val Val Ala Gly Val Thr Pro Tyr Ser His Val Ala Ile Phe Asp  
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Ser Asp Ala Gly Ser Gly Tyr Gly Trp Phe Leu Gly Gln Asn Gln Gly  
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Gly Ala Asn Gly Ala Tyr Asn Leu Val Lys Ile Pro Tyr Ser Thr Thr  
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Tyr Pro Thr Ala Phe Arg Pro Lys Val Phe Lys Asn Ala Val Thr Val  
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Ala Tyr Gln Gln Ala Asp Leu Thr Ala Thr Cys Gln Gln Ala Gly Thr  
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Thr Lys Thr Ile Ile Lys Val Ser Glu Ser Leu Ala Trp Leu Ser Asp  
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Arg His Gln Gln Gln Ala Asn Thr Ser Asp Pro Ile Gly Tyr Tyr His  
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Phe Gly Arg Phe Gly Gly Asp Ser Asn Leu Ala Gln Arg Glu Ala Asp  
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Leu Phe Leu Ser Asn Leu Pro Thr Lys Lys Val Ser Tyr Leu Val Ile  
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Val Ile Ala Phe Met Asp Lys Ile Ala Asn Ala Gly Tyr Lys Pro Val  
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Tyr Tyr Ser Tyr Lys Pro Phe Thr Leu Asn Asn Ile Asp Tyr Gln Gln  
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Tyr Glu Val Arg Thr Glu Pro Leu Trp Glu Phe Phe Pro Ser Met Asp  
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Thr Leu Arg Thr Asp Tyr Tyr Val Glu Ser Lys Pro Asn Ala Ser Ser  
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Ala Asp Lys Glu Phe Ile Lys Ala Gly Thr Arg Val Arg Val Tyr Glu  
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Lys Val Asn Gly Trp Ser Arg Ile Asn Ala Ser Gln Ser Asp Gln Trp  
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Val Glu Asp Lys Tyr Leu Ser Asn Ala Thr Gln Val  
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